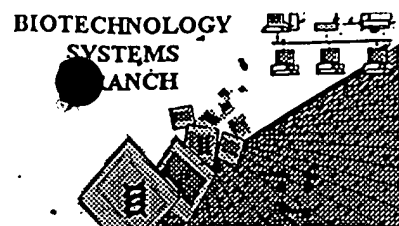


CRF



CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/759,112

Filing Date: 1/11/2001

Date Processed by STIC: 7/30/2001

STIC Contact: Mark Spencer, 703-308-4212

Nature of Problem:

The CRF (was):

☐ (circle one) Damaged or Unreadable (for Unreadable, see attached)

☐ Blank (no files on CRF) (see attached)

☐ Empty file (filename present, but no bytes in file) (see attached)

☐ Virus-infected. Virus name: _____ The STIC will not process the CRF.

☐ Not saved in ASCII text

☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should only be the Sequence Listing.

☒ Did not contain a Sequence Listing. (see attached sample)

☐ Other: _____

**PLEASE USE THE CHECKER VERSION 3.0 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR DETAILS:**

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Re-run

09/754, 112

```
`CDNASequence` 1F7 Heavy chain 5'
primer~mouse~actagtcgacatgaaatgcagctgggtcatsttcttc~flagctrym
kswbdhvn~DNA~yy~
`COtherFeature`
primer_bind 1F7 heavy chain 5'
primer~37~1~?~1F7 Heavy chain 3' primer~mouse
cccaagcttacgagggggaagacatttgggaa~flagctrymkswbdhvn
```

sample of submitted file =